



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: US/09/195,368B
Source: IFW16
Date Processed by STIC: 10-28-04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

US/09/195,368B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading!)
 (xi) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequences
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFW16

RAW SEQUENCE LISTING

DATE: 10/28/2004

PATENT APPLICATION: US/09/195,368B

TIME: 15:22:51

Input Set : A:\P1150R2.txt

Output Set: N:\CRF4\10282004\I195368B.raw

W--> 1 Patin Docket Preview - delete

7 <110> APPLICANT: Ashkenazi, Avi J.
 8 Baker, Kevin P.
 9 Godowski, Paul J.
 10 Gurney, Austin L.
 11 Mark, Melanie R.
 12 Marsters, Scot A.
 13 Pitti, Robert M.
 15 <120> TITLE OF INVENTION: DNA19355 Polypeptide, A Tumor Necrosis Factor Homolog
 17 <130> FILE REFERENCE: P1150R2
 19 <140> CURRENT APPLICATION NUMBER: US 09/195,368B
 20 <141> CURRENT FILING DATE: 1998-11-18
 22 <150> PRIOR APPLICATION NUMBER: US 60/069,661
 23 <151> PRIOR FILING DATE: 1997-12-12
 25 <150> PRIOR APPLICATION NUMBER: US 60/065,635
 26 <151> PRIOR FILING DATE: 1997-11-18
 28 <160> NUMBER OF SEQ ID NOS: 15
 30 <210> SEQ ID NO: 1
 31 <211> LENGTH: 177
 32 <212> TYPE: PRT
 33 <213> ORGANISM: Homo sapiens
 35 <400> SEQUENCE: 1
 36 Met Cys Leu Ser His Leu Glu Asn Met Pro Leu Ser His Ser Arg
 37 1 5 10 15
 39 Thr Gln Gly Ala Gln Arg Ser Ser Trp Lys Leu Trp Leu Phe Cys
 40 20 25 30
 42 Ser Ile Val Met Leu Leu Phe Leu Cys Ser Phe Ser Trp Leu Ile
 43 35 40 45
 45 Phe Ile Phe Leu Gln Leu Glu Thr Ala Lys Glu Pro Cys Met Ala
 46 50 55 60
 48 Lys Phe Gly Pro Leu Pro Ser Lys Trp Gln Met Ala Ser Ser Glu
 49 65 70 75
 51 Pro Pro Cys Val Asn Lys Val Ser Asp Trp Lys Leu Glu Ile Leu
 52 80 85 90
 54 Gln Asn Gly Leu Tyr Leu Ile Tyr Gly Gln Val Ala Pro Asn Ala
 55 95 100 105
 57 Asn Tyr Asn Asp Val Ala Pro Phe Glu Val Arg Leu Tyr Lys Asn
 58 110 115 120
 60 Lys Asp Met Ile Gln Thr Leu Thr Asn Lys Ser Lys Ile Gln Asn
 61 125 130 135
 63 Val Gly Gly Thr Tyr Glu Leu His Val Gly Asp Thr Ile Asp Leu
 64 140 145 150
 66 Ile Phe Asn Ser Glu His Gln Val Leu Lys Asn Asn Thr Tyr Trp

Does Not Comply
 Corrected Diskette Needed
 (Pg. 1, 3-4)

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TIME: 15:22:51

Input Set : A:\P1150R2.txt

Output Set: N:\CRF4\10282004\I195368B.raw

```

67          155          160          165
69 Gly Ile Ile Leu Leu Ala Asn Pro Gln Phe Ile Ser
70          170          175
72 <210> SEQ ID NO: 2
73 <211> LENGTH: 1964
74 <212> TYPE: DNA
75 <213> ORGANISM: Homo sapiens
77 <220> FEATURE:
78 <221> NAME/KEY: unsure
79 <222> LOCATION: 1857, 1875
80 <223> OTHER INFORMATION: n may be any nucleotide
82 <400> SEQUENCE: 2
83 cagctctcat ttctccaaaa atgtgtttga gccacttgga aaatatgcct 50
85 ttaagccatt caagaactca aggagctcag agatcatcct ggaagctgtg 100
87 gctcttttgc tcaatagtta tgttgctatt tctttgctcc ttcagttggc 150
89 taatctttat ttttctccaa ttagagactg ctaaggagcc ctgtatggct 200
91 aagtttggac cattaccctc aaaatggcaa atggcatctt ctgaacctcc 250
93 ttgctggaat aaggtgtctg actggaagct ggagatactt cagaatggct 300
95 tatatttaat ttatggccaa gtggctccca atgcaaacta caatgatgta 350
97 gctccttttg aggtgctggc gtataaaaac aaagacatga taaaaactct 400
99 aacaaacaaa tctaaaatcc aaaatgtagg agggacttat gaattgcatg 450
101 ttggggacac catagacttg atattcaact ctgagcatca ggttctaaaa 500
103 aataatacat actggggtat cattttacta gcaaattccc aattcatctc 550
105 ctagagactt gatttgatct cctcattccc ttcagcacat gtagagggtc 600
107 cagtgggttg attggagggg gaagatatct aatttctaga gtttgtctgt 650
109 ctacaaaaat caacacaaac agaactcctc tgcacgtgaa ttttcatcta 700
111 tcatgcctat ctgaaagaga ctgaggggaa gagccaaaga cttttggttg 750
113 gatctgcaga aatacttcat taatccatga taaaacaaat atggatgaca 800
115 gaggacatgt gcttttcaaa gaatctttat ctaattcttg aattcatgag 850
117 tggaaaaatg gagttctatt cccatggaag atttacctgg tatgcaaaaa 900
119 ggatctgggg cagtagcctg gctttgttct catattcttg ggctgctgta 950
121 attcattctt ctcatactcc catcttctga gaccctccca ataaaaagta 1000
123 gactgatagg atggccacag atatgcctac cataccctac tttagatatg 1050
125 gtggtgttag aagataaaga acaatctgag aactattgga atagaggtac 1100
127 aagtggcata aaatggaatg tacgctatct ggaaatttct cttggtttta 1150
129 tcttctcag gatgcagggt gctttaaaaa gccttatcaa aggagtcatt 1200
131 ccgaaccctc acgtagagct ttgtgagacc ttactgttgg tgtgtgtgtc 1250
133 taaacattgc taattgtaaa gaaagagtaa ccattagtaa tcattaggtt 1300
135 taaccccaga atggtattat cattactgga ttatgtcatg taatgattta 1350
137 gtatttttag ctagctttcc acagtttgca aagtgtcttc gtaaaacagt 1400
139 tagcaattct atgaagttaa ttgggcaggc atttggggga aaattttagt 1450
141 gatgagaatg tgataggcata gcatagccaa ctttctccta ctcataggac 1500
143 aagtgactac aagaggcaat gggtagtccc ctgcattgca ctgtctcagc 1550
145 tttagaattg ttatttctgc tatcgtgtta taagactcta aaacttagcg 1600
147 aattcacttt tcaggaagca tattccccct tagcccaagg tgagcagagt 1650
149 gaagctacaa cagatctttc ctttaccagc acaacttttt tttttttccc 1700
151 tgctgaatc agggagatcc aggatgctgt tcaggccaaa tcccaaccaa 1750
153 attccccctt tcaactttgc gggcccatct tagtcaaagt tgctaacttc 1800
155 taaaataata aatagcacta attcaaaatt tttggaatct taaattagct 1850

```

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Input Set : A:\P1150R2.txt

Output Set: N:\CRF4\10282004\I195368B.raw

W--> 157 acttgcnnggt tgcttggtga aaggnatata atgattacat tgtaaacaaa 1900
 159 tttaaaatat ttatggatat ttgtgaaaag ctgcattatg ttaaataata 1950
 161 ttacatgtaa agct 1964
 163 <210> SEQ ID NO: 3
 164 <211> LENGTH: 38
 165 <212> TYPE: DNA
 166 <213> ORGANISM: Unknown
 168 <220> FEATURE:

W--> 169 <221> NAME/KEY: Unknown Organism delete
 170 <222> LOCATION: 1-38
 171 <223> OTHER INFORMATION: Description of Unknown Organism: Unknown
 173 <400> SEQUENCE: 3
 174 gacgacaagc atatgtaga gactgctaag gagccctg 38
 176 <210> SEQ ID NO: 4
 177 <211> LENGTH: 34
 178 <212> TYPE: DNA
 179 <213> ORGANISM: Unknown
 181 <220> FEATURE:

W--> 182 <221> NAME/KEY: unknown organism delete
 183 <222> LOCATION: 1-34
 184 <223> OTHER INFORMATION: Description of Unknown Organism: Unknown
 186 <400> SEQUENCE: 4
 187 tagcagccgg atcctaggag atgaattggg gatt 34
 189 <210> SEQ ID NO: 5
 190 <211> LENGTH: 24
 191 <212> TYPE: PRT
 192 <213> ORGANISM: Unknown
 194 <220> FEATURE:

W--> 195 <221> NAME/KEY: unknown organism delete
 196 <222> LOCATION: 1-24
 197 <223> OTHER INFORMATION: Description of Unknown Organism: Unknown
 199 <400> SEQUENCE: 5
 200 Met Gly His His His His His His His His His Ser Ser Gly
 201 1 5 10 15
 203 His Ile Asp Asp Asp Asp Lys His Met
 204 20
 206 <210> SEQ ID NO: 6
 207 <211> LENGTH: 29
 208 <212> TYPE: DNA
 209 <213> ORGANISM: Unknown
 211 <220> FEATURE:

W--> 212 <221> NAME/KEY: unknown organism delete
 213 <222> LOCATION: 1-29
 214 <223> OTHER INFORMATION: Description of Unknown Organism: Unknown
 216 <400> SEQUENCE: 6
 217 atcagggact ttccgtggg gactttccg 29
 219 <210> SEQ ID NO: 7
 220 <211> LENGTH: 42
 221 <212> TYPE: DNA

Mandatory,
 if <213> response
 is Artificial
 Unknown, pls explain
 in section <220> -
 <223>.
 Invalid
 Response

Invalid
 Response

Invalid
 Response

Invalid
 Response

pls see item #
 on error
 summary sheet.
 10/28/04

RAW SEQUENCE LISTING

DATE: 10/28/2004

PATENT APPLICATION: US/09/195,368B

TIME: 15:22:51

Input Set : A:\P1150R2.txt

Output Set: N:\CRF4\10282004\I195368B.raw

```

222 <213> ORGANISM: Unknown
224 <220> FEATURE:
W--> 225 <221> NAME/KEY: unknown organism delete
226 <222> LOCATION: 1-42
227 <223> OTHER INFORMATION: Description of Unknown Organism: Unknown
229 <400> SEQUENCE: 7
230  tgtaaaacga cggccagttt ctctcagaga aacaagcaaa ac 42
232 <210> SEQ ID NO: 8
233 <211> LENGTH: 43
234 <212> TYPE: DNA
235 <213> ORGANISM: Unknown
237 <220> FEATURE:
W--> 238 <221> NAME/KEY: unknown organism delete
239 <222> LOCATION: 1-43
240 <223> OTHER INFORMATION: Description of Unknown Organism: Unknown
242 <400> SEQUENCE: 8
243  caggaaacag ctatgaccga agtggaccaa aggtctatcg cta 43
245 <210> SEQ ID NO: 9
246 <211> LENGTH: 126
247 <212> TYPE: PRT
248 <213> ORGANISM: Homo sapien
250 <400> SEQUENCE: 9
251  Glu Thr Ala Lys Glu Pro Cys Met Ala Lys Phe Gly Pro Leu Pro
252    1          5          10          15
254  Ser Lys Trp Gln Met Ala Ser Ser Glu Pro Pro Cys Val Asn Lys
255          20          25          30
257  Val Ser Asp Trp Lys Leu Glu Ile Leu Gln Asn Gly Leu Tyr Leu
258          35          40          45
260  Ile Tyr Gly Gln Val Ala Pro Asn Ala Asn Tyr Asn Asp Val Ala
261          50          55          60
263  Pro Phe Glu Val Arg Leu Tyr Lys Asn Lys Asp Met Ile Gln Thr
264          65          70          75
266  Leu Thr Asn Lys Ser Lys Ile Gln Asn Val Gly Gly Thr Tyr Glu
267          80          85          90
269  Leu His Val Gly Asp Thr Ile Asp Leu Ile Phe Asn Ser Glu His
270          95          100         105
272  Gln Val Leu Lys Asn Asn Thr Tyr Trp Gly Ile Ile Leu Leu Ala
273          110         115         120
275  Asn Pro Gln Phe Ile Ser
276          125
278 <210> SEQ ID NO: 10
279 <211> LENGTH: 150
280 <212> TYPE: PRT
281 <213> ORGANISM: Homo sapien
283 <400> SEQUENCE: 10
284  Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala
285    1          5          10          15
287  Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu
288          20          25          30

```

RAW SEQUENCE LISTING

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Input Set : A:\P1150R2.txt

Output Set: N:\CRF4\10282004\I195368B.raw

```

290  Ala Asn Gly Val  Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
291              35              40              45
293  Glu Gly Leu Tyr  Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln
294              50              55              60
296  Gly Cys Pro Ser  Thr His Val Leu Leu Thr His Thr Ile Ser Arg
297              65              70              75
299  Ile Ala Val Ser  Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile
300              80              85              90
302  Lys Ser Pro Cys  Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
303              95              100             105
305  Pro Trp Tyr Glu  Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
306              110             115             120
308  Lys Gly Asp Arg  Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu
309              125             130             135
311  Asp Phe Ala Glu  Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
312              140             145             150
314 <210> SEQ ID NO: 11
315 <211> LENGTH: 164
316 <212> TYPE: PRT
317 <213> ORGANISM: Homo sapien
319 <400> SEQUENCE: 11
320  Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg
321    1              5              10              15
323  Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu
324              20              25              30
326  Gly Arg Lys Ile  Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser
327              35              40              45
329  Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His
330              50              55              60
332  Glu Lys Gly Phe  Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe
333              65              70              75
335  Gln Glu Glu Ile  Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val
336              80              85              90
338  Gln Tyr Ile Tyr  Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu
339              95              100             105
341  Met Lys Ser Ala  Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr
342              110             115             120
344  Gly Leu Tyr Ser  Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu
345              125             130             135
347  Asn Asp Arg Ile  Phe Val Ser Val Thr Asn Glu His Leu Ile Asp
348              140             145             150
350  Met Asp His Glu  Ala Ser Phe Phe Gly Ala Gly Leu Val Gly
351              155             160
353 <210> SEQ ID NO: 12
354 <211> LENGTH: 141
355 <212> TYPE: PRT
356 <213> ORGANISM: Homo sapien
358 <400> SEQUENCE: 12
359  Glu Leu Arg Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg

```

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/195,368B

DATE: 10/28/2004
TIME: 15:22:52

Input Set : A:\P1150R2.txt
Output Set: N:\CRF4\10282004\I195368B.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; N Pos. 1857,1875 ✓

VERIFICATION SUMMARYPATENT APPLICATION: **US/09/195,368B**

DATE: 10/28/2004

TIME: 15:22:52

Input Set : **A:\P1150R2.txt**Output Set: **N:\CRF4\10282004\I195368B.raw**

L:1 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:
L:157 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:1850
L:169 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:182 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:195 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:212 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:225 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:238 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8